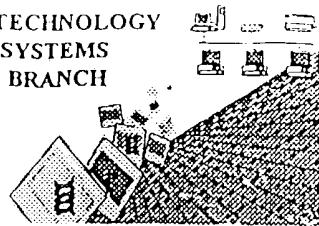


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/803, 580
Source: TFN0
Date Processed by STIC: 3/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/1/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1D03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER: 10/803,580

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic Acid Sequences The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IEWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt
 Output Set: N:\CRF4\03252004\J803580.raw

3 <110> APPLICANT: Syrrx, Inc.
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS
 7 <130> FILE REFERENCE: SYR-HDAC-5005-C2
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/803,580
 10 <141> CURRENT FILING DATE: 2004-03-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/455,437
 13 <151> PRIOR FILING DATE: 2003-03-17
 15 <150> PRIOR APPLICATION NUMBER: US 60/531,203
 16 <151> PRIOR FILING DATE: 2003-12-19
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 513
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Custom
 28 <220> FEATURE:
W--> 29 <221> NAME/KEY: Residues 1-482 of HDAC1 and a 6-histidine tag at the N-terminus
 30 <222> LOCATION: (1)..(513)
 32 <400> SEQUENCE: 1
 34 Met Ser Tyr Tyr His His His His His Asp Tyr Asp Ile Pro Thr
 35 1 5 10 15
 38 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
 39 20 25 30
 42 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp Gly
 43 35 40 45
 46 Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
 47 50 55 60
 50 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
 51 65 70 75 80
 54 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
 55 85 90 95
 58 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
 59 100 105 110
 62 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
 63 115 120 125
 66 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
 67 130 135 140
 70 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
 71 145 150 155 160
 74 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
 75 165 170 175
 78 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
 79 180 185 190

*INVALID (2137)
Response*

*Does Not Comply
Corrected Diskette Needed
(PG. 1-5)*

*Please see
item # 10
on error
summary
sheet.*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

82 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
 83 195 200 205
 86 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
 87 210 215 220
 90 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
 91 225 230 235 240
 94 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
 95 245 250 255
 98 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 99 260 265 270
 102 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
 103 275 280 285
 106 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
 107 290 295 300
 110 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
 111 305 310 315 320
 114 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr Ile
 115 325 330 335
 118 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
 119 340 345 350
 122 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
 123 355 360 365
 126 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
 127 370 375 380
 130 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
 131 385 390 395 400
 134 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
 135 405 410 415
 138 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
 139 420 425 430
 142 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
 143 435 440 445
 146 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys Asn
 147 450 455 460
 150 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
 151 465 470 475 480
 154 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
 155 485 490 495
 158 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
 159 500 505 510
 162 Ala
 166 <210> SEQ ID NO: 2
 167 <211> LENGTH: 1542
 168 <212> TYPE: DNA
 169 <213> ORGANISM: Custom *INVALID (2137)*
 170 <214> *Response*
 171 <220> FEATURE:
 W--> 173 <221> NAME/KEY: DNA sequence encoding residues 1-482 of HDAC1 and a 6-histidine
 W--> 174 tag at the N-terminus
 175 <222> LOCATION: (1)..(1542)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004
TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt
Output Set: N:\CRF4\03252004\J803580.raw

177 <400> SEQUENCE: 2
 178 atgtcgtaactaccatcac gattacgata tcccaacgac cgaaaacctg 60
 180 tattttcagg gcgcacatgg accccgggga tccatggcgc agacgcaggg caccggagg 120
 182 aaagtctgtt actactacga cggggatgtt gaaattact attatggaca aggccaccca 180
 184 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tcttaccga 240
 186 aaaatggaaa tctatcgccc tcacaaagcc aatgtctgagg agatgaccaa gtaccacagc 300
 188 gatgactaca ttaaattctt gcgcctccatc cgtccagata acatgtcgga gtacagcaag 360
 190 cagatgcaga gattcaacgt tggtgaggac tgtccagtt tcgatggct gttttagttc 420
 192 tgtcgttgtt ctactgggtt ttctgtggca agtgcgtgtga aacttaataa gcagcagacg 480
 194 gacatcgctg tgaattgggc tgggggcctg caccatgca aagaagtccga ggcacatctggc 540
 196 ttctgttacg tcaatgatat cgtcttggcc atccttggaa tgcataaagta tcaccagagg 600
 198 gtgcgttaca ttgacattga tattcaccat ggtgacggcg tggaaagaggg cttctacacc 660
 200 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720
 202 gacctacggg atatcgggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780
 204 gacgggattt atgacgagtc ctatgaggcc atttcaagc cggcatgtc caaagtaatg 840
 206 gagatgttcc agcctagtgc ggtggctt cagtggtggct cagactccct atctgggat 900
 208 cggtaggtt gcttaatct aactatcaa ggacacgcca agtgtgtgga atttgtcaag 960
 210 agctttaacc tgcctatgct gatgtgggaa ggcgggtgtt acaccattcg taacgttgcc 1020
 212 cggctgttga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080
 214 tacaatgact actttgaata ctttggacca gattcaagc tccacatcag tccttccaat 1140
 216 atgactaacc agaacacgaa ttagtacctg gagaagatca aacagcgtact gttttagaaac 1200
 218 cttagaatgc tgccgcacgc acctggggc caaatgcagg cgattcctga ggacccatc 1260
 220 cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcacatc gatctgtcc 1320
 222 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380
 224 gccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaaa 1440
 226 gagaagagcc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500
 228 ccagaagcca aagggtcaa ggaggaggc aagtggcct ga 1542

231 <210> SEQ ID NO: 3

232 <211> LENGTH: 498

233 <212> TYPE: PRT

234 <213> ORGANISM: Custom

237 <220> FEATURE:

INVALID (213)
Response

W--> 238 <221> NAME/KEY: Residues 1-488 of HDAC2 and a 6-histidine tag at the C-terminus

239 <222> LOCATION: (1)..(498)

241 <400> SEQUENCE: 3

243	Met	Gly	Ser	Met	Ala	Tyr	Ser	Gln	Gly	Gly	Gly	Lys	Lys	Lys	Val	Cys
244	1					5				10				15		
247	Tyr	Tyr	Tyr	Asp	Gly	Asp	Ile	Gly	Asn	Tyr	Tyr	Tyr	Gly	Gln	Gly	His
248							20			25				30		
251	Pro	Met	Lys	Pro	His	Arg	Ile	Arg	Met	Thr	His	Asn	Leu	Leu	Leu	Asn
252							35			40				45		
255	Tyr	Gly	Leu	Tyr	Arg	Lys	Met	Glu	Ile	Tyr	Arg	Pro	His	Lys	Ala	Thr
256							50			55				60		
259	Ala	Glu	Glu	Met	Thr	Lys	Tyr	His	Ser	Asp	Glu	Tyr	Ile	Lys	Phe	Leu
260	65						70				75			80		
263	Arg	Ser	Ile	Arg	Pro	Asp	Asn	Met	Ser	Glu	Tyr	Ser	Lys	Gln	Met	Gln
264							85			90				95		
267	Arg	Phe	Asn	Val	Gly	Glu	Asp	Cys	Pro	Val	Phe	Asp	Gly	Leu	Phe	Glu
268							100			105				110		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004
TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt
Output Set: N:\CRF4\03252004\J803580.raw

271 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
 272 115 120 125
 275 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
 276 130 135 140
 279 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
 280 145 150 155 160
 283 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
 284 165 170 175
 287 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
 288 180 185 190
 291 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
 292 195 200 205
 295 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
 296 210 215 220
 299 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
 300 225 230 235 240
 303 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
 304 245 250 255
 307 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
 308 260 265 270
 311 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
 312 275 280 285
 315 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
 316 290 295 300
 319 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
 320 305 310 315 320
 323 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
 324 325 330 335
 327 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
 328 340 345 350
 331 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
 332 355 360 365
 335 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
 336 370 375 380
 339 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
 340 385 390 395 400
 343 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
 344 405 410 415
 347 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
 348 420 425 430
 351 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
 352 435 440 445
 355 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
 356 450 455 460
 359 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Lys Thr Asp Thr
 360 465 470 475 480
 363 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
 364 485 490 495
 367 His His

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt
 Output Set: N:\CRF4\03252004\J803580.raw

371 <210> SEQ ID NO: 4
 372 <211> LENGTH: 1497
 373 <212> TYPE: DNA
 374 <213> ORGANISM: Custom
 377 <220> FEATURE:

-Invalid (213) response

W--> 378 <221> NAME/KEY: DNA sequence encoding residues 1-488 of HDAC2 and a 6-histidine tag at the C-terminus

380 <222> LOCATION: (1)..(1497)
 382 <400> SEQUENCE: 4

383 atgggatcca tggcgtagag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac	60
385 ggtgatattt gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc	120
387 atgaccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc	180
389 cataaagcca ctgccagaaga aatgacaaa tatcacagtg atgagtttat caaatttcta	240
391 cggtaataa gaccagataa catgtctgag tatacatagc agatgcagag atttaatgtt	300
393 ggagaagatt gtccagtgtt tgatggactc tttgagttt gtcagcttc aactggcggt	360
395 tcagttctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattggct	420
397 ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgtatatt	480
399 gtgcttgcca tccttgaatt actaaagtat catcagagag tcttataatat tgatataat	540
401 attcatcatg gtgatgggt tgatggactg ttttatacaa cagatcgatg aatgacggta	600
403 tcattccata aatatgggaa atactttcct ggcacaggag acttgaggaa tattgggtct	660
405 gaaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgatca	720
407 tatggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgt	780
409 gtggattac agtgtggc agactcattt tctgtgtata gactgggtt tttcaatcta	840
411 acagtcaaag gtcatgctaa atgtgtgaa gttgtaaaaa cttttaactt accattactg	900
413 atgcttggag gaggtggcta cacaatccgt aatgttgc tgcgttggac atatggact	960
415 gcagttgcc ttgattgtga gattccaaat gagttgccccat ataatgatta cttttagtat	1020
417 tttggaccag acttcaaact gcatattatg ctttcaaaaca tgacaaacca gaacactcca	1080
419 gaatatatgg aaaagataaaa acagcgttt tttgaaaatt tgccatgtt acctcatgca	1140
421 cctgggtgtcc agatgcaagc tattccagaa gatgtgttc atgaagacag tggagatgaa	1200
423 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagttgt	1260
425 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaaa tgtggctgt	1320
427 cataagaaaag gagcaaagaa agctagaattt gaagaagata agaaagaaaac agaggacaaa	1380
429 aaaacagacg ttaaggaaga agataaaatcc aaggacaaca gtggtaaaaa aacagatacc	1440
431 aaaggaaacca aatcagaaca gtcagcaac cccggccatc accatcacca tcaactaa	1497

434 <210> SEQ ID NO: 5

435 <211> LENGTH: 782

436 <212> TYPE: PRT

437 <213> ORGANISM: Custom

440 <220> FEATURE:

-Invalid (213) Response

W--> 441 <221> NAME/KEY: Residues 73-845 of HDAC6 and a 6-histidine tag at the C-terminus

442 <222> LOCATION: (1)..(782)

444 <400> SEQUENCE: 5

446 Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr			
447 1	5	10	15
450 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp			
451	20	25	30
454 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln			
455	35	40	45
458 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg			



The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/803,580

DATE: 03/25/2004

TIME: 17:07:52

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:174 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:2
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:379 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:441 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:650 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6
L:742 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:854 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:855 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:8